

SEQUENCE LISTING

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INABE, Kazunori

<120> CAP BINDING PROTEIN

<130> Q87392

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<160> 26

<170> PatentIn version 3.3

<210> 1

<211> 528

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(525)

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cgg	tcc	ggg	gcc	tcc	gcg	gcc	ccc	gcg	gcc	tcc	gcg	gcc	gct	gcc	ttg	96
Arg	Ser	Gly	Ala	Ser	Ala	Ala	Pro	Ala	Ala	Ser	Ala	Ala	Ala	Ala	Leu	
		20					25						30			

gca	ccc	agc	gcc	acc	cgc	aca	cgg	cgc	tcc	gct	agc	cag	gcc	ggg	agc	144
Ala	Pro	Ser	Ala	Thr	Arg	Thr	Arg	Arg	Ser	Ala	Ser	Gln	Ala	Gly	Ser	
		35					40					45				

aag	agc	cag	gcg	gtg	gag	aag	ccg	ccg	tcg	gag	aag	ccg	ccg	ctg	agg	192
Lys	Ser	Gln	Ala	Val	Glu	Lys	Pro	Pro	Ser	Glu	Lys	Pro	Arg	Leu	Arg	
	50					55					60					

cgc	tcg	tcg	ccg	cgg	gcc	cag	gag	gag	ggc	ccg	ggg	gag	ccg	ccg	ccg	240
Arg	Ser	Ser	Pro	Arg	Ala	Gln	Glu	Glu	Gly	Pro	Gly	Glu	Pro	Pro	Pro	
65					70				75					80		

cct	gag	ctg	gcg	ttg	ctc	ccg	cca	ccg	ccg	ccg	ccg	ccg	ccg	act	ccc	288
Pro	Glu	Leu	Ala	Leu	Leu	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Thr	Pro	
			85					90						95		

gcg	acc	ccg	acg	tcc	tcg	gcg	tcc	aac	ctg	gac	ctg	ggc	gag	cag	cgg	336
Ala	Thr	Pro	Thr	Ser	Ser	Ala	Ser	Asn	Leu	Asp	Leu	Gly	Glu	Gln	Arg	
			100					105					110			

gag cgc tgg gag acg ttc cag aag cgg cag aag ctt acc tcc gag ggt 384
 Glu Arg Trp Glu Thr Phe Gln Lys Arg Gln Lys Leu Thr Ser Glu Gly
 115 120 125

gcc gcc aag ctc ctg cta gac acc ttt gaa tac cag ggc ctg gtg aag 432
 Ala Ala Lys Leu Leu Leu Asp Thr Phe Glu Tyr Gln Gly Leu Val Lys
 130 135 140

cac aca gga ggc tgc cac tgt gga gca gtt cgt ttt gaa gtt tgg gcc 480
 His Thr Gly Gly Cys His Cys Gly Ala Val Arg Phe Glu Val Trp Ala
 145 150 155 160

tca gca gac ttg cat ata ttt gac tgc aag tac cgg aat tat ata tga 528
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 165 170 175

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 <213> Homo sapiens

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Arg Ser Gly Ala Ser Ala Ala Pro Ala Ala Ser Ala Ala Ala Leu
 20 25 30

Ala Pro Ser Ala Thr Arg Thr Arg Arg Ser Ala Ser Gln Ala Gly Ser
 35 40 45

Lys Ser Gln Ala Val Glu Lys Pro Pro Ser Glu Lys Pro Arg Leu Arg
 50 55 60

Arg Ser Ser Pro Arg Ala Gln Glu Glu Gly Pro Gly Glu Pro Pro Pro
 65 70 75 80

Pro Glu Leu Ala Leu Leu Pro Pro Pro Pro Pro Pro Pro Thr Pro
 85 90 95

Ala Thr Pro Thr Ser Ser Ala Ser Asn Leu Asp Leu Gly Glu Gln Arg
 100 105 110

Glu Arg Trp Glu Thr Phe Gln Lys Arg Gln Lys Leu Thr Ser Glu Gly
 115 120 125

Ala Ala Lys Leu Leu Leu Asp Thr Phe Glu Tyr Gln Gly Leu Val Lys
 130 135 140

His Thr Gly Gly Cys His Cys Gly Ala Val Arg Phe Glu Val Trp Ala
 145 150 155 160

Ser Ala Asp Leu His Ile Phe Asp Cys Lys Tyr Arg Asn Tyr Ile
 165 170 175

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 Arg Ser Gly Ala Ser Gly Ala Ser Ala Ala Pro Ala Ala Ser Ala Ala
 20 25 30
 gct gcc ttg gca ccc agc gcc acc cgc aca cgg cgc tcc gct agc cag 144
 Ala Ala Leu Ala Pro Ser Ala Thr Arg Thr Arg Arg Ser Ala Ser Gln
 35 40 45
 gcc ggg agc aag agc cag gcg gtg gag aag ccg ccg tcg gag aag ccg 192
 Ala Gly Ser Lys Ser Gln Ala Val Glu Lys Pro Pro Ser Glu Lys Pro
 50 55 60
 cgg ctg agg cgc tcg tcg ccg cgg gcc cag gag gag ggc ccg ggg gag 240
 Arg Leu Arg Arg Ser Ser Pro Arg Ala Gln Glu Glu Gly Pro Gly Glu
 65 70 75 80
 ccg ccg ccg cct gag ctg gcg ttg ctc ccg cca ccg ccg ccg ccg ccg 288
 Pro Pro Pro Pro Glu Leu Ala Leu Leu Pro Pro Pro Pro Pro Pro Pro
 85 90 95
 ccg act ccc gcg acc ccg acg tcc tcg gcg tcc aac ctg gac ctg ggc 336
 Pro Thr Pro Ala Thr Pro Thr Ser Ser Ala Ser Asn Leu Asp Leu Gly
 100 105 110
 gag cag cgg gag cgc tgg gag acg ttc cag aag cgg cag aag ctt acc 384
 Glu Gln Arg Glu Arg Trp Glu Thr Phe Gln Lys Arg Gln Lys Leu Thr
 115 120 125
 tcc gag ggt gcc gcc aag ctc ctg cta gac acc ttt gaa tac cag ggc 432
 Ser Glu Gly Ala Ala Lys Leu Leu Leu Asp Thr Phe Glu Tyr Gln Gly
 130 135 140
 ctg gtg aag cac aca gga ggc tgc cac tgt gga gca gtt cgt ttt gaa 480
 Leu Val Lys His Thr Gly Gly Cys His Cys Gly Ala Val Arg Phe Glu
 145 150 155 160

ggt tgg gcc tca gca gac ttg cat ata ttt gac tgc aag tac cgg aat 528
 Val Trp Ala Ser Ala Asp Leu His Ile Phe Asp Cys Lys Tyr Arg Asn
 165 170 175

tat ata tga 537
 Tyr Ile

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<400> 4

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 20 25 30

Ala Ala Leu Ala Pro Ser Ala Thr Arg Thr Arg Arg Ser Ala Ser Gln
 35 40 45

Ala Gly Ser Lys Ser Gln Ala Val Glu Lys Pro Pro Ser Glu Lys Pro
 50 55 60

Arg Leu Arg Arg Ser Ser Pro Arg Ala Gln Glu Glu Gly Pro Gly Glu
 65 70 75 80

Pro Pro Pro Pro Glu Leu Ala Leu Leu Pro Pro Pro Pro Pro Pro Pro
 85 90 95

Pro Thr Pro Ala Thr Pro Thr Ser Ser Ala Ser Asn Leu Asp Leu Gly
 100 105 110

Glu Gln Arg Glu Arg Trp Glu Thr Phe Gln Lys Arg Gln Lys Leu Thr
 115 120 125

Ser Glu Gly Ala Ala Lys Leu Leu Leu Asp Thr Phe Glu Tyr Gln Gly
 130 135 140

Leu Val Lys His Thr Gly Gly Cys His Cys Gly Ala Val Arg Phe Glu
 145 150 155 160

Val Trp Ala Ser Ala Asp Leu His Ile Phe Asp Cys Lys Tyr Arg Asn
 165 170 175

Tyr Ile

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atag 64

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<210> 26
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tcaggaggag ttagtgaggg



20